D1

wherein the double-stranded region comprises the constant sequence and the single-stranded region comprises the random sequence.

D2

3.   (Amended) The method of claim 113, wherein C is between about 7-20 nucleotides and R is between about 3-5 nucleotides.

4.   (Amended) The method of claim 113, wherein the array contains about 4^R different probes.

D3

70.   (Amended) An array of nucleic acid probes, wherein each probe has a double-stranded portion, a single stranded portion, and a random nucleotide sequence of length R within the single-stranded portion.

71.   (Amended) The array of claim 70 comprising about 4^R different nucleic acid probes.

D4

80.   (Amended) A method for detecting a target nucleic acid in a sample comprising:

a)   contacting the array of probes with the sample, wherein each probe has a double-stranded portion, a single-stranded portion, and a random sequence within the single-stranded portion; and

b)   identifying hybrids, whereby the target nucleic acid is detected.

D5

89.   (Amended) A solid support, comprising an array of nucleic acid probes, wherein each probe has a double-stranded portion, a single-stranded portion, and a random sequence of length R within the single-stranded portion.

Please add claims 111-122 as follows.

D6

111.   A method for creating an array of probes, comprising:

a)   synthesizing a first set of nucleic acids each comprising a constant sequence and a random sequence of length R;

b)   synthesizing a second set of nucleic acids each comprising a sequence complementary to the constant sequence of the first nucleic acid; and

c)   hybridizing the first set of nucleic acids with the second set of nucleic acids, whereby the probes in the array have a double-

-2-

D6

stranded region and a single-stranded region, and

wherein the single-stranded region comprises the random sequence.

112. The method of claim 111, wherein the array contains about 4^R different probes.

113. A method for creating an array of probes, comprising:

a) synthesizing a first set of nucleic acids each comprising a constant sequence of length C at a 3' terminus and a random sequence of length R at a 5' terminus;

b) synthesizing a second set of nucleic acids each comprising a sequence complementary to the constant sequence of the first nucleic acid; and

c) hybridizing the first set of nucleic acids with the second set of nucleic acids, whereby the probes in the array have a double-stranded region and a single-stranded region, and

wherein the single-stranded region comprises the random sequence.

114. An array of nucleic acid probes, wherein each probe has a double-stranded portion comprising a constant sequence, a single-stranded portion and a random nucleotide sequence within the single-stranded portion.

115. The array of claim 70 containing less than 4^R nucleic acid probes, wherein the number of nucleic acid probes contained within the array is such that the number of random sequences within the array permits determination of the nucleotide sequence of a target nucleic acid by hybridization of the target nucleic acid or fragments thereof to the array.

116. A solid support, comprising an array of nucleic acid probes, wherein each probe has a double-stranded portion comprising a constant sequence, a single-stranded portion, and a random sequence within the single-stranded portion.

117. The method of claim 95, wherein the random sequence is of length R.

D6

118. The method of claim 95, wherein the double-stranded portion comprises a constant sequence.

119. The method of claim 110, wherein the random sequence is of length R.

120. The method of claim 110, wherein the double-stranded portion comprises a constant sequence.

121. The method of claim 80, wherein the random sequence is of length R.

Concluded

122. The method of claim 80, wherein the double-stranded portion comprises a constant sequence.

REMARKS

Any fees that may be due in connection with filing this paper or with this application may be charged to Deposit Account No. 50-1213. If a Petition for extension of time is required, this paper is to be considered such Petition, and any fee charged to Deposit Account No. 50-1213.

Claims 1-5 and 65-122 are pending. Claims 1, 3, 4, 70, 71, 80 and 89 have been amended and claims 111-122 have been added. Basis for the amendments can be found throughout the specification and claims as originally filed. For example, basis for amendment of claim 1 can be found on page 21, line 1, page 30, line 4, and page 31, lines 5-6. Basis for claims 111 and 112 can be found, for example, on page 20, lines 14-17, and page 21, lines 1 and 25-27. Basis for claim 113 can be found, for example, on page 20, line 29, through page 21, line 4.

Included, per 37 C.F.R. § 1.121., as an attachment is a marked-up version of the claims that are amended.

THE REJECTION OF CLAIMS 1-5 AND 65-110 UNDER 35 U.S.C. 103(a)

Claims 1-5 and 65-110 are rejected under 35 U.S.C. §103(a) as allegedly being unpatentable over Khrapko *et al.* [(1991) *J. DNA Sequencing and Mapping* *1*:375-388] in view of Drmanac *et al.* [(1990) *DNA and Cell Biol.* *9*:527-534].